which may contribute to the vascular leakage in DHF/DSS.

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Molecular characterization of dengue virus from Nepal

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Background: Dengue is a global health problem and its expanding endemicity towards new territories is a serious concern. Relatively a new disease in Nepalese context, dengue abruptly appeared as massive outbreak in 2010, merely four years after its first introduction. We report the first phylogenetic relationship of the dengue virus type 1 (DENV-1) strains from Nepal based on the complete envelop (*E*) gene sequences.

Methods: During 2010 outbreak, specimens of 1215 clinical dengue cases from central and western Nepal were tested for IgG/IgM by enzyme linked immuno-sorbent assay (ELISA). Maintaining the original proportion of ELISA positive and negative cases (approximately 1:2), 282 specimens (about one-fourth) were selected by random sampling and further analyzed by reverse transcription-polymerase chain reaction (RT-PCR). Complete *E* gene (1485bp) sequencing of DENV-1 strains was performed and phylogenetic tree of Nepalese strains was created together with 38 global *E* gene sequences of DENV-1 retrieved from GenBank.

Results: Of 1215 clinical cases, 29.5% (359) and 70.5% were found dengue positive and negative respectively (ratio about 1:2) by ELISA. Out of 282 sampled for molecular investigation, RT-PCR detected 90 (31.9%) cases including 44 (15.6%) cases previously negative by ELISA. Detection rate increased to 45.4% (128/282) with the combination of ELISA and RT-PCR. All four serotypes were confirmed with DENV-1 as the major one (64.4%) responsible for this outbreak. Phylogenetic analysis of the *E* gene sequences of 32 DENV-1 strains from Nepal clustered into genotype V. Nepalese DENV-1 strains showed close similarity with the recent strains from India and Singapore.

Conclusion: Over dependency on single serological test (mostly rapid) has led to underestimation of dengue burden in the country. Moreover, co-circulation of all serotypes possesses a threat for severe dengue outbreaks in the future. Due to the lack of dengue sequence data from Nepal, we could not shape the exact evolutionary dynamics and origin of the virus in the country. Nevertheless, we have generated nucleotide sequence database for better understanding of molecular epidemiology in the country. India may be the origin of Nepalese dengue virus strains based on the close genetic similarity observed and extensive cross-border activities.

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Endogenous interferon-gamma response in chronic hepatitis C Egyptian patients treated with peginterferon plus ribavirin

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Background: Hepatits C virus (HCV) infections remains an increasingly prevalent and emergent health problem worldwide that causes a wide spectrum of liver diseases. Combination therapy with pegylated interferon (peginterferon) and ribavirin is currently recognized as the standard treatment of chronic hepatitis C. Several immunological mechanisms are involved in the course of treatment of HCV via interferons. Data are rare in the literature on the role of endogenous interferon gamma in Egyptian patients with chronic hepatitis C treated with pegylated interferon and ribavirin therapy. The present study was thus conducted to evaluate the role of endogenous IFNγ in the response of chronic hepatitis C (CHC) patients following treatment with pegylated plus ribavirin.

Methods: Forty patients with chronic hepatitis C (CHC) infection were included in the study. Twenty healthy blood donors were used as healthy control. Human peripheral blood mononuclear cells (PBMCs) were prepared and cultured. IFNγ secretion from PBMC/ml was determined in 24 hr culture supernatants, using standard protocols for sandwich enzyme linked immunosorbant assay (ELISA). The biallelic G/T polymorphism in the promoter region of MxA at position – 88 from the transcription start site [17] was genotyped using restriction fragment length polymorphism (RFLP).

Results: It was found that enhanced IFNγ production would be predicted to favor HCV clearance. Our finding that the magnitude of pretreatment of interferon alpha (IFNα)-driven IFNγ responses correlates with initial response to therapy is certainly consistent with this prediction. In addition, our findings suggested that the single nucleotide polymorphism (SNP) of the MxA gene is one of the important host factors that independently influences the response to IFNα in patients with CHC infection, especially those with a low viral load.

Conclusion: In conclusion, enhanced IFNγ production would be predicted to favor HCV clearance. Our finding that the magnitude of pretreatment of alpha IFN-driven IFNγ responses correlates with initial response to therapy is certainly consistent with this prediction. Our findings suggested that the SNP of the MxA gene is one of the important host factors that independently influences the response to alpha IFN in patients with chronic HCV infection, especially those with a low viral load.

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